REMARKS

This amendment is submitted in an earnest effort to bring this application to issue without delay.

The Examiner has accepted Applicants' submission of the certified English translation of the German priority document and so he has dropped his application of the BELL et al reference, applied in the previous office action as a basis to find that Applicants' claims lack a common technical feature justifying the examination of all claims together in one application and as a basis for arguing that the prior art anticipates the presently claimed invention. The Examiner therefore indicates on page 3, first full paragraph of the office action, that he will rejoin claims 1 through 10 and 27 through 29, but he has withdrawn claims 11 through 26 from further consideration on the grounds that Applicants have presented no allowable generic claim in this application. The Examiner now justifies withdrawing claims 11 through 26 on the grounds that newly cited US Patent 6,037,154 to SUGA et al discloses the modification of a nucleic acid to express a deregulated 3-phosphoglycerate dehydrogenase in Corynebacteria to reduce feedback inhibition.

Applicants do not agree with the Examiner's objections to the specification set forth on pages 4 and 5 of the office action in which the Examiner requests that Applicants provide a new sequence listing in both paper form and computer-readable form. The sequence listing and Statement Under 37 CFR 1.821(f) and (g)

provided with Applicants' Preliminary Amendment of 3 May 2005 in both computer readable form on a disk and in paper form adequately fulfills all of the requirements of the rules. Perhaps the Examiner has overlooked Applicants' submission of the sequence listing. Applicants checked the US Patent and Trademark Office PAIRS Data Base, and see that the correct sequence listing has been included in the file under document SEQLIST entered 3 May 2005. The only possible basis for objection that Applicants can find is that when Applicants amended the specification on page 29, to assign Sequence Numbers 13 through 19 to the seven primer sequences, Applicants inserted the sequence numbers altogether near the bottom of page 28, and not next to each of the individual seven sequences as they appear in the specification on pages 27 and 28. In the present amendment Applicants specifically added in parentheses, the sequence number after each individual primer sequence.

Nonetheless in order to expedite prosecution of this application, Applicants have filed electronically on 16 March 2009, an electronic, computer-readable version of the sequence listing as well as a Statement Under 37 CFR 1.821(f) and (g) that the sequence listing information contains no new matter.

Next, Applicants have amended the claims 1 through 26, 28 and 29 on file to remove all improper multiple dependencies and other informalities pointed out by the Examiner. Applicants have canceled claim 27. By making the amendments to the claims, Applicants have:

1. Removed all multiple dependencies not in compliance with US practice;

2. Removed the objections to the claims set forth by the Examiner on page 5 of the office action;

3. Removed the bases for rejection of the claims under 35 USC 112, second paragraph, as indefinite as set forth on pages 5 and 6 of the office action;

4. Removed the Examiner's rejection of the claims under 35 USC 112, first paragraph, on the grounds that the claims are based on a specification whose description of the invention and the examples do not provide an adequate description of the invention to show that the Applicants had possession of the invention as presently claimed at the time the application was filed, and

5. Removed the bases for the Examiner's rejection of the claims as anticipated under 35 USC 102 by the SUGA et al US Patents 6,037,154 and 6,258,573.

Applicants do not agree with the Examiner, however, that the word "and" in claim 28, step (a) before "selected from the group consisting of" should be deleted since deletion of the "and" makes it unclear whether the SEQ ID NOS. 1 through 5 refer to the nucleic acids encoding the deregulated 3-phosphoglycerate dehydrogenases or to the deregulated 3-phosphoglycerate dehydrogenases themselves. Of course the Seq ID NOS. 1 through 5 are nucleic acid sequences, and not polypeptide sequences.

Applicants note that the Examiner has placed a most important passage in the office action at the end on page 12 under the heading CONCLUSION when he states that the nucleic acid sequences SEQ ID NOS. 1 through 5 and the polypeptide sequences SEQ ID NOS. 7 through 11 are not taught by the prior art, including the two SUGA et al patents. The Examiner's statement indicates that the Examiner believes that the application discloses allowable subject matter and that he may be willing to allow claims directed to the allowable subject matter so long as the claims are not too broad to either be indefinite, be beyond the scope of the invention described in the specification, and do not come too close to the invention disclosed in SUGA et al. The Examiner has focused on the terms in claims 1 through 5, in particular allele, homolog, derivative of a nucleotide sequence or nucleotide sequence hybridizing therewith. The Examiner believes that these expressions are all indefinite because there are no boundaries provided to adequately define the scope of these terms. The Examiner believes that these terms are also not supported by the scope of the invention as defined or as enabled by the specification since the Applicants have provided only a limited number of examples and a limited number of specific nucleic acid sequences that express the deregulated 3-phosphoglycerate dehydrogenase, as well as a limited number of the deregulated amino acid sequences that are expressed by the nucleic acid and that have reduced feedback inhibition to catalyze the dehydrogenation of

2-phosphoglycerate to facilitate synthesis of L-serine while at the same time not hurting the yield of the L-serine through feedback inhibition.

Most importantly the Examiner expresses his concern that the nucleic acid of SEQ ID NO. 13 as defined in each of the two SUGA et al patents, obtained from Coryneform bacteria, and the deregulated amino acid of SEQ ID NO. 14 expressed by the nucleic acid of SEQ ID NO. 13 and having reduced feedback inhibition comes too close to the nucleic acid defined in claims 1 through 5 and too close to the amino acid sequences defined in claims 11 through 15 to patentably distinguish over SUGA et al. In fact, because of the broad definitions of allele, homolog, derivative of a nucleotide sequence or nucleotide sequence hybridizing therewith, the Examiner even argues that SEQ ID NO. 13 in the SUGA et al patents anticipates claims 1 through 5 and SEQ ID NO. 14 in the two SUGA et al patents anticipates claims 11 through 15.

Applicants emphasize that SEQ ID NO: 13 in the two SUGA et al patents is structurally far removed from the SEQ ID NOS. 1 through 5 in the present application first of all because the SEQ ID NO. 13 expresses a deregulated 3-phosphoglycerate dehydrogenase that in position 325 has an amino acid residue that is not Glu as in the wild type, but is instead Lys in particular. When the SUGA et al invention is considered more broadly than the sequences that are SEQ

ID NOS. 13 and 14, then the amino acid residue in the position 325 is more broadly defined as any amino acid other than Glu, the naturally occurring amino acid residue in that position. Applicants note that the amino acid sequences SEQ ID NOS. 7 through 10 in the present invention have no such substitution in the amino acid residue at position 325. The SEQ ID NO. 11 according to the invention has the C-terminal amino acids cut off to include the amino acid residue at position 325. Thus none of the amino acid sequences in the present application or the nucleic acid sequences that express these amino acid sequences comes structurally close to the nucleic acid sequences or amino acid sequences disclosed in the reference.

The Examiner is apparently concerned that the broad definition of alleles, homologs, derivatives and hybridizing sequences could include nucleic acid sequences which express amino acid sequences where the Glu in position 325 is replaced by Lys. The Examiner argues that SEQ ID NO. 13 in the SUGA et al patents could be considered an allele, homolog, derivative of or sequence hybridizing with any of SEQ ID NOS. 1 through 5 in the present application.

Applicants do not agree with the Examiner's broad interpretation of the SUGA et al references and specifically deny that the reference provides any basis to reject any of the claims in

this application as last presented under 35 USC 102 as anticipated. Nonetheless, in the interest of obtaining allowance of the claims Applicants are limiting the claims to cover in claims 1 through 10, only the nucleotides of SEQ ID NOS. 1 through 5. Thus the references provide no basis to reject any of the claims under 35 USC 102 as anticipated or 35 USC 103 as obvious.

Applicants now ask that the Examiner rejoin claims 11 through 26 with the claims presently examined now that Applicants believe that they have submitted claims 1 through 10 directed to nucleic acids that are allowable over SUGA et al and that the claims no longer include any improper multiple dependencies. Applicants note that claims 11 through 19 are directed to the polypeptides of the SEQ ID NOS. 7, 8, 9, 10 and 11, which are the polypeptides expressed by the structurally novel and unobvious polynucleotides of SEQ ID NOS. 1 through 5. Applicants find no disclosure or suggestion in either of the SUGA et al references of polypeptides having the structures of SEQ ID NOS. 7 through 11. Thus the references provide no basis to reject any of the claims under 35 USC 102 as anticipated or 35 USC 103 as obvious.

Claims 20, 21, and 23 through 25, are directed to microorganisms that contain one or more of the polynucleotides of SEQ ID NOS. 1 through 5, and claim 22 is directed to microorganisms that express at least one amino acid sequence having SEQ ID NOS. 7

through 11. There is no disclosure or suggestion of such polynucleotides or polypeptides to be found in the SUGA et al references. Thus the references provide no basis to reject any of the claims under 35 USC 102 as anticipated or 35 USC 103 as obvious.

Claim 26 is directed to a series of probes having SEQ ID NOS. 13 through 19, which are used for identifying the polynucleotides of SEQ ID NOS. 1 through 5 that encode the polypeptides that participate in the biosynthesis of L-serine, including the polypeptides of SEQ ID NOS. 7 through 11. Applicants find no disclosure or suggestion of these probes in the SUGA et al references. Thus the references provide no basis to reject claim 26 under 35 USC 102 as anticipated or 35 USC 103 as obvious.

Claims 28 and 29 are directed to a method of microbially producing L-serine from a carbohydrate, fat or oil which comprises expressing Coryneform bacteria transformed with a polynucleotide having SEQ ID NOS. 1, 2, 3, 4 or 5, which are expressed to form a deregulated 3-phosphoglycerate dehydrogenase, employing the deregulated enzyme to catalyze the microbial production of L-serine, and isolating the L-serine. Once again there is no disclosure or suggestion in the two SUGA et al references to prepare L-serine using the Coryneform bacteria, transformed with a polynucleotide having SEQ ID NOS. 1, 2, 3, 4 or 5, and which are expressed to form a deregulated 3-phosphoglycerate dehydrogenase

used to catalyze the microbial production of L-serine. Thus the references provide no basis to reject claims 28 and 29 under 35 USC 102 as anticipated or 35 USC 103 as obvious.

Applicants believe that all claims now presented are allowable and a response to that effect is earnestly solicited.

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Enclosure:
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